

RAW SEQUENCE LISTING

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Application Serial Number: 09/619,30C
Source: IFW16
Date Processed by STIC: 3/8/05

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/619,310C

DATE: 03/08/2005

TIME: 10:36:33

Input Set : A:\2005-01-02 4614-0140PUS1.ST25.txt
 Output Set: N:\CRF4\03082005\I619310C.raw

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3 <110> APPLICANT: THASTRUP, Ole
4     TULLIN, Soren
5     POULSEN, Lars K
6     BJORN, Sara P
8 <120> TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
10 <130> FILE REFERENCE: 4614-0140PUS1
12 <140> CURRENT APPLICATION NUMBER: US 09/619,310C
13 <141> CURRENT FILING DATE: 2000-07-19
15 <150> PRIOR APPLICATION NUMBER: US 08/819,612
16 <151> PRIOR FILING DATE: 1997-03-17
18 <150> PRIOR APPLICATION NUMBER: PCT/DK96/00051
19 <151> PRIOR FILING DATE: 1996-01-31
21 <150> PRIOR APPLICATION NUMBER: DK 1065/95
22 <151> PRIOR FILING DATE: 1995-09-22
25 <160> NUMBER OF SEQ ID NOS: 23
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 36
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: GFP2 primer directed to A. victoria
37 <400> SEQUENCE: 1
38 tggaaataagg ttatgagta aaggagaaga actttt                               36
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42 <211> LENGTH: 36
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: GFP-1 primer directed to A. victoria
49 <400> SEQUENCE: 2
50 aagaattcgg atcccttttag tgtcaattgg aagtct                               36
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 67
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: 5' PCR primer incorporating the Y66H substitution responsible
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60     changing green fluorescence into blue fluorescence
62 <400> SEQUENCE: 3
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65 gatacc
68 <210> SEQ ID NO: 4                               67

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69 <211> LENGTH: 36
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: 3' PCR primer incorporating the Y66H substitution responsible
for
75      changing green fluorescence into blue fluorescence
77 <400> SEQUENCE: 4
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81 <210> SEQ ID NO: 5
82 <211> LENGTH: 30
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
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93 <210> SEQ ID NO: 6
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: 3' primer used to flank the Y66H-GFP
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102 cttcgttt gaattcggat cccttagtg          30
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106 <211> LENGTH: 48
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment and ligated to SEQ ID NO:8
113 <400> SEQUENCE: 7
114 catggccaac gcttgcact actctctttt atgggtttca atgctttt          48
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 48
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: synthetic NcoI-XbaI DNA linker and ligated to SEQ ID NO:7
125 <400> SEQUENCE: 8
126 ctagaaaagc attgaacacc ataagagaga gtagtgacaa gcgttggc          48
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 48
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment ligated to SEQ ID NO:10
137 <400> SEQUENCE: 9
138 catggccaac gcttgcact actctcactt atgggtttca atgctttt          48
141 <210> SEQ ID NO: 10

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142 <211> LENGTH: 48
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Ncol-Xba1 DNA linker ligated to SEQ ID NO:9
149 <400> SEQUENCE: 10
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154 <211> LENGTH: 36
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: 5' primer based on pGFP-N1 plasmid
161 <400> SEQUENCE: 11
162 tggaaaatgc tttatggata aaggagaaga actttt 36
165 <210> SEQ ID NO: 12
166 <211> LENGTH: 35
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: 3' primer based on pGFP-N1 plasmid
173 <400> SEQUENCE: 12
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177 <210> SEQ ID NO: 13
178 <211> LENGTH: 40
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: 5' primer based on pZeoSV-LacZ plasmid
185 <400> SEQUENCE: 13
186 tggaaaatgc tttatggatc ccgtcgaaaa acaacgtcgt 40
189 <210> SEQ ID NO: 14
190 <211> LENGTH: 34
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: 3' primer based on pZeoSV-LacZ plasmid
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201 <210> SEQ ID NO: 15
202 <211> LENGTH: 764
203 <212> TYPE: DNA
204 <213> ORGANISM: Aequorea Victoria
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (8)..(721)
211 <400> SEQUENCE: 15
212 aagcttt atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att 49
213 Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile

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214	1	5	10	
216	ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt			97
217	Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser			
218	15	20	25	30
220	gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt			145
221	Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
222	35	40	45	
224	att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act			193
225	Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
226	50	55	60	
228	act ttc tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg			241
229	Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
230	65	70	75	
232	aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag			289
233	Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
234	80	85	90	
236	gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct			337
237	Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
238	95	100	105	110
240	gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa			385
241	Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
242	115	120	125	
244	ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa			433
245	Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu			
246	130	135	140	
248	tac aac tat aac tca cat aat gta tac atc atg gca gac aaa cca aag			481
249	Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys			
250	145	150	155	
252	aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga			529
253	Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly			
254	160	165	170	
256	agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat			577
257	Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
258	175	180	185	190
260	ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc			625
261	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
262	195	200	205	
264	ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag			673
265	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu			
266	210	215	220	
268	ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa			721
269	Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
270	225	230	235	
272	taaatgtcca gacttccaaat tgacactaaa gggatccgaa ttc			764
275	<210> SEQ ID NO: 16			
276	<211> LENGTH: 238			
277	<212> TYPE: PRT			
278	<213> ORGANISM: Aequorea Victoria			
280	<400> SEQUENCE: 16			

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282 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
283 1      5          10          15
286 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
287 20      25          30
290 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
291 35      40          45
294 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
295 50      55          60
298 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
299 65      70          75          80
302 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
303 85      90          95
306 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
307 100     105         110
310 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
311 115     120         125
314 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
315 130     135         140
318 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
319 145     150         155         160
322 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
323 165     170         175
326 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
327 180     185         190
330 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
331 195     200         205
334 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
335 210     215         220
338 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
339 225     230         235
342 <210> SEQ ID NO: 17
343 <211> LENGTH: 764
344 <212> TYPE: DNA
345 <213> ORGANISM: Aequorea victoria
348 <220> FEATURE:
349 <221> NAME/KEY: CDS
350 <222> LOCATION: (8)..(724)
352 <400> SEQUENCE: 17
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355     1      5          10
357 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt      97
358 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
359 15      20          25          30
361 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      145
362 Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
363     35      40          45
365 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      193
366 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

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VERIFICATION SUMMARY DATE: 03/08/2005
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